

10/677,977

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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Sep 05 15:35:32 EDT 2007

=====

Reviewer Comments:

<210> 6

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<221> Variant

<222> (1)..(1)

<223> Wherein Xaa is an N-acetyl group.

<220>

<221> Variant

<222> (6)..(6)

<223> Wherein Xaa is a 7-amino-4-methylcoumarin group.

<400> 6

Xaa Ile Glu Pro Asp Xaa

1

5

The above explanations for Xaa are invalid: "Xaa" can only represent a
single amino acid, not a functional group.

<210> 29

<211> 4

<212> PRT

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<220>
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The above <223> explanation for "Xaa" at location 4 contains a misspelling: please replace "ot" with "or."

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<220>
<223> Cathepsin F substrate spec.

<220>

Validated By CRFValidator v 1.0.3

Application No: 10677977

Version No: 4.0

Input Set:

Output Set:

Started: 2007-08-23 14:48:11.063
Finished: 2007-08-23 14:48:11.915
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 852 ms
Total Warnings: 3
Total Errors: 3
No. of SeqIDs Defined: 57
Actual SeqID Count: 57

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 257	Invalid sequence data feature in <221> in SEQ ID (22)
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E 341	'Xaa' position not defined SEQID (54) POS (2)

SEQUENCE LISTING

<110> Nguyen, Jack
 Thanos, Chris
 Waugh Ruggles, Sandra
 Craik, Charles S.

<120> METHODS OF GENERATING AND SCREENING FOR PROTEASES WITH ALTERED
 SPECIFICITY

<130> 19049-005001/4905

<140> 10677977

<141> 2003-10-02

<150> 60/425,388

<151> 2002-10-02

<160> 57

<170> FastSEQ for Windows Version 4.0

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<211> 277

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Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
 20 25 30

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
 35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
 50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
 65 70 75 80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
 85 90 95

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
 100 105 110

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<400> 6

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130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Asp Ala Asp
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
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His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
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Leu Tyr Phe Tyr His
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The above "<222> 3" is an incorrect location for "Xaa:" "Leu" is at location 3; "Xaa" is at location 2.

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Lys Tyr Ala Asp

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<211> 4

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Asn Gly Pro Lys

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<211> 4

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Gly Thr Ser Asp

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Ala Gln Glu Lys

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Arg Ile Asp Tyr

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Xaa Xaa Xaa Arg

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<220>

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<223> Xaa= Phe or Lys

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Xaa Xaa Xaa Xaa

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Xaa.Xaa Xaa Xaa

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Xaa Xaa Xaa Arg

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<220>

<221> VARIANT

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Xaa Xaa Pro Arg

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<210> 35

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Xaa Xaa Leu Xaa

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